

SEQUENCE LISTING

<110> Mendel Biotechnology, Inc.  
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 SHERMAN, Bradley K

<120> PLANT TRANSCRIPTIONAL REGULATORS OF ABIOTIC STRESS

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 <151> 2003-04-10

<150> 09/533,030  
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<150> 09/837,944  
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<150> 10/171,468  
 <151> 2002-06-14

<150> 60/310,847  
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<150> 60/336,049
<151> 2001-11-19

<150> Polynucleotides and Polypeptides in Plants
<151> 2003-09-18

<150> 60/434,166
<151> 2002-12-17

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<170> PatentIn version 3.2

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cctatagcta atatcagcag gatcatgaag aaagcggtgc ctccaatgg taagattgga      240
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35 40 45

Ala Lys Asp Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile  
50 55 60

Thr Ser Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Val  
65 70 75 80

Asn Gly Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu Asp  
85 90 95

Tyr Leu Glu Pro Leu Lys Ile Tyr Leu Ala Arg Tyr Arg Glu Leu Glu  
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ccggatcatg aagaaggcct tgcccgccaa cgccaagatc tctaaagatg ccaaagagac	360
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          20           25           30

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Pro Ile Ala Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn
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Ala Lys Ile Ser Lys Asp Ala Lys Glu Thr Met Gln Glu Cys Val Ser
          50           55           60

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Glu Phe Ile Ser Phe Val Thr Gly Glu Ala Ser Asp Lys Cys Gln Lys
65           70           75           80

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Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr
          85           90           95

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Thr Leu Gly Phe Glu Asp Tyr Val Glu Pro Leu Lys Val Tyr Leu Gln
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Arg Phe Arg Glu Ile Glu Gly Glu Arg Thr Gly Leu Gly Arg Pro Gln
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Thr Gly Gly Glu Val Gly Glu His Gln Arg Asp Ala Val Gly Asp Gly  
130 135 140

Gly Gly Phe Tyr Gly Gly Gly Gly Gly Met Gln Tyr His Gln His His  
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Ser Asp Ser Gly Gly Gly Ala Ala Ser Gly Arg Thr Arg Thr  
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gcgaacgcaa aaatctctaa ggatgctaaa gaaacgggttc aagagtgtgt atcggaattc 180  
ataagtttca tcaccggtga ggcttctgac aagtgtcaga gagagaagag gaagacaatc 240  
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ctcaaggttt atctgcaaaa gtataggag gtggaaggag agaagactac tacggcaggg 360  
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Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile Ser Lys Asp  
35 40 45

Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile  
50 55 60

Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr Ile  
65 70 75 80

Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly Phe Glu Asp  
85 90 95

Tyr Val Glu Pro Leu Lys Val Tyr Leu Gln Lys Tyr Arg Glu Val Glu  
100 105 110

Gly Glu Lys Thr Thr Thr Ala Gly Arg Gln Gly Asp Lys Glu Gly Gly  
115 120 125

Gly Gly Gly Gly Gly Ala Gly Ser Gly Ser Gly Gly Ala Pro Met Tyr  
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Gly Gly Gly Met Val Thr Thr Met Gly His Gln Phe Ser His His Phe  
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gacacaaaagg gatcagcaaa aggtggggat ccaaagcga agaaagatgg gcaatcaagc 420  
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Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Arg Gly Leu  
35 40 45

Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu Ile Val Gln Glu  
50 55 60

Cys Val Ser Glu Phe Ile Ser Phe Val Thr Ser Glu Ala Ser Asp Lys  
65 70 75 80

Cys Gln Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp  
85 90 95

Ala Met Ala Thr Leu Gly Phe Glu Asp Tyr Met Glu Pro Leu Lys Val  
100 105 110

Tyr Leu Met Arg Tyr Arg Glu Gly Asp Thr Lys Gly Ser Ala Lys Gly  
115 120 125

Gly Asp Pro Asn Ala Lys Lys Asp Gly Gln Ser Ser Gln Asn Gly Gln  
130 135 140

Phe Ser Gln Leu Ala His Gln Gly Pro Tyr Gly Asn Ser Gln Val Thr  
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Phe Pro Leu Phe Ser Ser His Ser Ser Asn Thr His His Ser Leu Leu  
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Phe	Leu	Pro	Ile	Ala	Asn	Ile	Ser	Arg	Ile	Met	Lys	Arg	Gly	Leu	Pro
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Leu	Asn	Gly	Lys	Ile	Ala	Lys	Asp	Ala	Lys	Glu	Thr	Met	Gln	Glu	Cys
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Gln Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala  
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Met Ala Thr Leu Gly Phe Glu Asp Tyr Ile Asp Pro Leu Lys Val Tyr  
100 105 110

Leu Met Arg Tyr Arg Glu Met Glu Gly Asp Thr Lys Gly Ser Gly Lys  
115 120 125

Gly Gly Glu Ser Ser Ala Lys Arg Asp Gly Gln Pro Ser Gln Val Ser  
130 135 140

Gln Phe Ser Gln Val Pro Gln Gln Gly Ser Phe Ser Gln Gly Pro Tyr  
145 150 155 160

Gly Asn Ser Gln Ser Leu Arg Phe Gly Asn Ser Ile Glu His Leu Glu  
165 170 175

Val Leu Met Ser Ser Thr Arg Thr Leu Phe Ile Thr Ile Phe Arg Asp  
180 185 190

Ser Thr Met Pro Val Val Ser Glu Asn Leu Ser Asp Pro Leu Ser Ile  
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Leu Ser Cys Lys  
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tccggctagc ccaggcggcg gcagccacga gagcggcgac cacagccctc gctctaacgt 300  
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ccctgttggtc tgaatccatc aggcggcttg gtaaagaccg agattttagg actgattgta     1020
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 20 25 30

Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Gly  
 35 40 45

Lys Ile Ala Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu  
 50 55 60

Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Asp Lys Cys Gln Arg Glu  
 65 70 75 80

Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Ala Thr  
 85 90 95

MBI-0022CIP.ST25.txt

Leu Gly Phe Glu Asp Tyr Met Asp Pro Leu Lys Ile Tyr Leu Thr Arg  
100 105 110

Tyr Arg Glu Met Glu Gly Asp Thr Lys Gly Ser Ala Lys Gly Gly Asp  
115 120 125

Ser Ser Ala Lys Arg Asp Val Gln Pro Ser Pro Asn Ala Gln Leu Ala  
130 135 140

His Gln Gly Ser Phe Ser Gln Asn Val Thr Tyr Pro Asn Ser Gln Gly  
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Arg His Met Met Val Pro Met Gln Gly Pro Glu  
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Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala Leu  
 35 40 45

Pro Pro Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu Thr Val Gln Glu  
 50 55 60

Cys Val Ser Glu Phe Ile Ser Phe Val Thr Ser Glu Ala Ser Asp Lys  
 65 70 75 80

Cys Gln Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp  
 85 90 95

Ala Met Thr Thr Leu Gly Phe Glu Glu Tyr Ile Asp Pro Leu Lys Val  
 100 105 110

Tyr Leu Ala Ala Tyr Arg Glu Ile Glu Gly Asp Ser Lys Gly Ser Ala  
 115 120 125

Lys Gly Gly Asp Ala Ser Ala Lys Arg Asp Val Tyr Gln Ser Pro Asn  
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Gly Gln Val Ala His Gln Gly Ser Phe Ser Gln Gly Val Asn Tyr Thr  
 145 150 155 160

Asn Ser

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20          25          30

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35          40          45

Lys Ile Ser Lys Glu Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu
50          55          60

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Phe Ile Ser Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Lys Glu  
65 70 75 80

Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr  
85 90 95

Leu Gly Phe Glu Asp Tyr Val Asp Pro Leu Lys Ile Tyr Leu His Lys  
100 105 110

Tyr Arg Glu Met Glu Gly Glu Lys Thr Ala Met Met Gly Arg Pro His  
115 120 125

Glu Arg Asp Glu Gly Tyr Gly His Gly His Gly His Ala Thr Pro Met  
130 135 140

Met Thr Met Met Met Gly His Gln Pro Gln His Gln His Gln His Gln  
145 150 155 160

His Gln His Gln His Gln Gly His Val Tyr Gly Ser Gly Ser Ala Ser  
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Ser Ala Arg Thr Arg  
180

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<223> n is a, c, g, or t

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ttctcccat agcgaacgtg agcaggatca tgaagaaggc cttgccggcg aacgcgaaga 180  
tctcgaagga cgcgaaggag acggtgcagg aatgcgtgtc ggagttcatc agcttcataa 240  
cgggtgaggc gtcggacaag tgccagaggg agaagcgcaa gaccatcaac ggcgacgac 300  
ttctctgggc catgacaacc ctgggattcg aagagtacgt ggagcctctg aagatttacc 360  
tccagcgctt ccgcgagatg gagggagaga agaccgtggc cgcccgcgac tcttctaagg 420

MBI-0022CIP.ST25.txt

actcggcctc cgcctcctcc tatcatcagg gacacgtgta cggctcccct gcctaccatc 480  
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ctttgcaaga tcaactgggtt 620

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Ser Gly Asn Leu Ser Glu Leu Ser Pro Arg Glu Gln Asp Arg Phe Leu  
20 25 30

Pro Ile Ala Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn  
35 40 45

Ala Lys Ile Ser Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser  
50 55 60

Glu Phe Ile Ser Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg  
65 70 75 80

Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr  
85 90 95

Thr Leu Gly Phe Glu Glu Tyr Val Glu Pro Leu Lys Ile Tyr Leu Gln  
100 105 110

Arg Phe Arg Glu Met Glu Gly Glu Lys Thr Val Ala Ala Arg Asp Ser  
115 120 125

Ser Lys Asp Ser Ala Ser Ala Ser Ser Tyr His Gln Gly His Val Tyr  
130 135 140

Gly Ser Pro Ala Tyr His His Gln Val Pro Gly Pro Thr Tyr Pro Ala  
145 150 155 160

Pro Gly Arg Pro Arg  
165

<210> 19  
 <211> 1872  
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<200>  
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ttctccttat atttattaaa ctataatata gtatatataa agaaaagatt ttgagaattt      180
gaataaaata agagtgtcca agtcagaggc gagcacgtgc cagataccaa agcaacggtc      240
cagatcatgg agcactcacc aaatccaagg gctcctattt gtccgtgcaa actcacactt      300
atcgcccaac aacggtccac aaagcgccac gtgtttctca gataaagcgt tattaaccct      360
tctgatccaa cggatcctgc tcattacctc ccaaacaagc ccttccgttc cgtttcacct      420
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gaacaagttt cttccgttaa cagcacttca acttcacgtg gaacaagaat caaacggttt      900
cgtgggttcg attctcaatt cctcgtccat tcgcaatcga ttttcaaatt ccgaagaaaa      960
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ctgccggcga acgcgaagat ctccaaggac gcgaaggaga cgggtgcagga gtgcgtgtcg     1320
gagttcatca gtttcatcac cggcgaggcc tccgacaagt gccagcggga gaagcgcaag     1380
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gagcctctca agggctacct ccagcgcttc cgagaaatgg aaggagagaa gaccgtggcg     1500
gcgcgtgaca aggacgcgcc tcctcctacc aatgctacca acagtgccta cgagagtcct     1560
    
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MBI-0022CIP.ST25.txt

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tccaatgccg gtaggccag gtagatgggc ctatgttatt attattatta ttattcttat 1740
tcgtaagtta aaagaaatgt gagattcaaa gtggtgatta agtgaattag taacaaaaaa 1800
gtgcgactca gttgattaaa aatatatata aattattata agtcttttaa tatgtttttg 1860
attctcacac at 1872

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<211> 188
<212> PRT
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<200>
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1          5          10          15

Gly Ser Glu Met Ser Pro Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala
          20          25          30

Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile
          35          40          45

Ser Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile
          50          55          60

Ser Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg
65          70          75          80

Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly
          85          90          95

Phe Glu Asp Tyr Val Glu Pro Leu Lys Gly Tyr Leu Gln Arg Phe Arg
          100          105          110

Glu Met Glu Gly Glu Lys Thr Val Ala Ala Arg Asp Lys Asp Ala Pro
          115          120          125

Pro Pro Thr Asn Ala Thr Asn Ser Ala Tyr Glu Ser Pro Ser Tyr Ala
          130          135          140

Ala Ala Pro Gly Gly Ile Met Met His Gln Gly His Val Tyr Gly Ser
145          150          155          160

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Ala Gly Phe His Gln Val Ala Gly Gly Ala Ile Lys Gly Gly Pro Val  
 165 170 175

Tyr Pro Gly Pro Gly Ser Asn Ala Gly Arg Pro Arg  
 180 185

<210> 21  
 <211> 521  
 <212> DNA  
 <213> Glycine max

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 agggagcaag acaggttcct tccgatagcg aacgtgagca ggatcatgaa gaaggcggtg 180  
 ccggcgaaac cgaagatctc gaaggaggcg aaggagacgg tgcaggagtg cgtgtcggag 240  
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 <222> (158)..(158)  
 <223> Xaa can be any naturally occurring amino acid

<200>  
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<400> 22

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Gly Ser Asn Glu Phe Ser Gly Cys Arg Glu Gln Asp Arg Phe Leu Pro  
 20 25 30

MBI-0022CIP.ST25.txt

Ile Ala Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala  
35 40 45

Lys Ile Ser Lys Glu Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu  
50 55 60

Phe Ile Ser Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Lys Glu  
65 70 75 80

Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr  
85 90 95

Leu Gly Phe Glu Glu Tyr Val Glu Pro Leu Lys Val Tyr Leu His Lys  
100 105 110

Tyr Arg Glu Leu Glu Gly Glu Lys Thr Ala Met Met Gly Arg Pro His  
115 120 125

Glu Arg Asp Glu Gly Tyr Gly His Ala Thr Pro Met Met Ile Met Met  
130 135 140

Gly His Gln Gln Gln Gln His Gln Gly His Val Tyr Gly Xaa  
145 150 155

<210> 23  
<211> 556  
<212> DNA  
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<200>  
<223> G3471 GLYMA-28NOV01-CLUSTER4778\_1

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acatcagccg cattatgaag aaggctctgc ctcccaacgg caagattgca aaggatgcca 180  
aagacaccat gcaggaatgc gtttctgagt tcatcagctt cattaccagc gaggcgagtg 240  
agaaatgccga gaaggagaag agaaagacaa tcaatggaga cgatttgcta tgggccatgg 300  
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aagttggcct tgcaggtcaa aattctcagc ttgttcatca gggttcgctg aactatattg 480  
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gatgcttcta cgcac 556

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 <211> 173  
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<200>  
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<400> 24

Met Ser Asp Ala Pro Pro Ser Pro Thr His Glu Ser Gly Gly Glu Gln  
 1 5 10 15

Ser Pro Arg Gly Ser Ser Ser Gly Ala Arg Glu Gln Asp Arg Tyr Leu  
 20 25 30

Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala Leu Pro Pro Asn  
 35 40 45

Gly Lys Ile Ala Lys Asp Ala Lys Asp Thr Met Gln Glu Cys Val Ser  
 50 55 60

Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Glu Lys Cys Gln Lys  
 65 70 75 80

Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Ala  
 85 90 95

Thr Leu Gly Phe Glu Asp Tyr Ile Glu Pro Leu Lys Val Tyr Leu Ala  
 100 105 110

Arg Tyr Arg Glu Ala Glu Gly Asp Thr Lys Gly Ser Ala Arg Ser Gly  
 115 120 125

Asp Gly Ser Ala Thr Pro Asp Gln Val Gly Leu Ala Gly Gln Asn Ser  
 130 135 140

Gln Leu Val His Gln Gly Ser Leu Asn Tyr Ile Gly Leu Gln Val Gln  
 145 150 155 160

Pro Gln His Leu Val Met Pro Ser Met Gln Ser His Glu  
 165 170

<210> 25  
 <211> 939  
 <212> DNA  
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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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ctctttgtca ccgggtttgt gagatgtcgg atgcaccggc gagtccgagt cacgagagtg 180  
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cccttgaatg cttgtacgca tggcatgggt ggaaccaatt gtctggtaaa aaaatggggg 720  
ggctctcgtc ccccggggtg ggggggtttt gtttcggtac tngtngnt tttnttaaa 780  
acacgncttg tagcgggtgt ttctcttctc aaggagaga tgtgttagg gttatgctag 840  
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<222> (151)..(151)  
<223> Xaa can be any naturally occurring amino acid

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Ser Pro Arg Gly Ser Leu Ser Gly Ala Ala Arg Glu Gln Asp Arg Tyr  
20 25 30

Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala Leu Pro Pro  
35 40 45

Asn Gly Lys Ile Ala Lys Asp Ala Lys Asp Thr Met Gln Glu Cys Val  
50 55 60

Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Glu Lys Cys Gln  
65 70 75 80

Lys Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met  
85 90 95

Ala Thr Leu Gly Phe Glu Asp Tyr Ile Glu Pro Leu Lys Val Tyr Leu  
100 105 110

Ala Arg Tyr Arg Glu Ala Glu Gly Asp Thr Lys Gly Ser Ala Arg Ser  
115 120 125

Gly Asp Gly Ser Ala Arg Pro Asp Gln Val Gly Leu Ala Gly Gln Asn  
130 135 140

Ala Gln Val Gln Pro Gln Xaa Ser Gly Tyr Ala Phe Asn Ala Arg Pro  
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<210> 27  
<211> 1231  
<212> DNA

<213> Oryza sativa

<200>

<223> ORYSA-22JAN02-CLUSTER26105\_1

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tatgcctccc aatacagatt atatggaacc gaatgacagc caaagaccaa ttgttaaatt      180
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tccatgagaa ccaagtacat cctttttcac agagccatca ccagcctttg cagttaattt      600
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<400> 28

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Ser Gly Ser Pro Arg Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
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Gly Gly Pro Leu Val Arg Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile  
35 40 45

Ser Arg Ile Met Lys Lys Ala Ile Pro Ala Asn Gly Lys Ile Ala Lys  
50 55 60

Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe  
65 70 75 80

Ile Thr Ser Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr  
85 90 95

Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu  
100 105 110

Asp Tyr Ile Glu Pro Leu Lys Val Tyr Leu Gln Lys Tyr Arg Glu Met  
115 120 125

Glu Gly Asp Ser Lys Leu Thr Ala Lys Ala Gly Asp Gly Ser Val Lys  
130 135 140

Lys Asp Val Leu Gly Ser His Gly Gly Ser Ser Ser Ser Ala Gln Gly  
145 150 155 160

Met Gly Gln Gln Ala Ala Tyr Asn Gln Gly Met Gly Tyr Met Gln Pro  
165 170 175

Gln Tyr His Asn Gly Asp Val Ser Asn  
180 185

<210> 29  
<211> 229  
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<213> Oryza sativa

<200>  
<223> OSC12630.C1.p5.fg polypeptide

<400> 29

Met Pro Asp Ser Asp Asn Glu Ser Gly Gly Pro Ser Asn Ala Gly Glu  
1 5 10 15

Tyr Ala Ser Ala Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Val  
20 25 30



MBI-0022CIP.ST25.txt

Ser Arg Ile Met Lys Arg Ala Leu Pro Ala Asn Ala Lys Ile Ser Lys  
35 40 45

Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe  
50 55 60

Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr  
65 70 75 80

Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly Phe Glu  
85 90 95

Asp Tyr Ile Asp Pro Leu Lys Leu Tyr Leu His Lys Phe Arg Glu Leu  
100 105 110

Glu Gly Glu Lys Ala Ile Gly Ala Ala Gly Ser Gly Gly Gly Gly Ala  
115 120 125

Ala Ser Ser Gly Gly Ser Gly Ser Gly Ser Gly Ser His His His Gln  
130 135 140

Asp Ala Ser Arg Asn Asn Gly Gly Tyr Gly Met Tyr Gly Gly Gly Gly  
145 150 155 160

Gly Met Ile Met Met Met Gly Gln Pro Met Tyr Gly Ser Pro Pro Ala  
165 170 175

Ser Ser Ala Gly Tyr Ala Gln Pro Gln Pro Pro His His His His His  
180 185 190

Gln Met Val Met Gly Gly Lys Gly Lys Val Glu Glu Val Gln Ser Lys  
195 200 205

Gly Lys Ile Arg Asp Phe Leu Gln Leu Gln Ala Ser Met Leu Glu Leu  
210 215 220

Ile Gln Gly Glu Asn  
225

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<200>  
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<400> 30

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20 25 30

Gly Arg Ile Met Arg Arg Ala Val Pro Glu Asn Gly Lys Ile Ala Lys  
35 40 45

Asp Ser Lys Glu Ser Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe  
50 55 60

Ile Thr Ser Glu Ala Ser Asp Lys Cys Leu Lys Glu Lys Arg Lys Thr  
65 70 75 80

Ile Asn Gly Asp Asp Leu Ile Trp Ser Met Gly Thr Leu Gly Phe Glu  
85 90 95

Asp Tyr Val Glu Pro Leu Lys Leu Tyr Leu Arg Leu Tyr Arg Glu Gly  
100 105 110

Asp Thr Lys Gly Ser Arg Ala Ser Glu Leu Pro Val Lys Lys Asp Val  
115 120 125

Val Leu Asn Gly Asp Pro Gly Ser Ser Leu Val Asn Tyr Gly Ala Gln  
130 135 140

Arg Ala Asp Ala Asn Ala Asn His Leu Asp Leu Phe Phe Leu Leu Arg  
145 150 155 160

Lys Asn Pro Glu Ser Thr Thr Ala Asn Cys Met Arg Glu Asp Glu Ala  
165 170 175

Lys Pro Val Thr Val Lys Ile Ile Glu Thr Val Tyr Val Glu Ala Asp  
180 185 190

Thr Ala Asp Asp Phe Lys Ser Val Val Gln Arg Leu Thr Gly Lys Asp  
195 200 205

Ala Val Ala Gly Asp Ala Pro Glu Leu Asn Ser Ala Gln Arg Phe Gly  
210 215 220

Ser Gly Arg Glu Ala Ser Arg His Gly Asp His Lys Val Arg Ile Tyr  
225 230 235 240

Glu

<210> 31  
 <211> 297  
 <212> PRT  
 <213> Oryza sativa

<200>  
 <223> OSC30077.C1.p6.fg polypeptide  
 <400> 31

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 20 25 30

Gly Gly Gly Gly Cys Gly Ser Ser Ala Gly Tyr Val Val Tyr Gly Gly  
 35 40 45

Gly Gly Gly Gly Asp Ser Pro Ala Lys Glu Gln Asp Arg Phe Leu Pro  
 50 55 60

Ile Ala Asn Val Ser Arg Ile Met Lys Arg Ser Leu Pro Ala Asn Ala  
 65 70 75 80

Lys Ile Ser Lys Glu Ser Lys Glu Thr Val Gln Glu Cys Val Ser Glu  
 85 90 95

Phe Ile Ser Phe Val Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu  
 100 105 110

Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr  
 115 120 125

Leu Gly Phe Glu Ala Tyr Val Gly Pro Leu Lys Ser Tyr Leu Asn Arg  
 130 135 140

Tyr Arg Glu Ala Glu Gly Glu Lys Ala Asp Val Leu Gly Gly Ala Gly  
 145 150 155 160

Gly Ala Ala Ala Ala Arg His Gly Glu Gly Gly Cys Cys Gly Gly Gly  
 165 170 175

Gly Gly Gly Ala Asp Gly Val Val Ile Asp Gly His Tyr Pro Leu Ala  
 180 185 190

Gly Gly Leu Ser His Ser His His Gly His Gln Gln Gln Asp Gly Gly

195

200

205

Gly Asp Val Gly Leu Met Met Gly Gly Gly Asp Ala Gly Val Gly Tyr  
210 215 220

Asn Ala Gly Ala Gly Ser Thr Thr Thr Ala Phe Tyr Ala Pro Ala Ala  
225 230 235 240

Thr Ala Ala Ser Gly Asn Lys Ala Tyr Cys Gly Gly Asp Gly Ser Arg  
245 250 255

Val Met Glu Phe Glu Gly Ile Gly Gly Glu Glu Glu Ser Gly Gly Gly  
260 265 270

Gly Gly Gly Gly Glu Arg Gly Phe Ala Gly His Leu His Gly Val Gln  
275 280 285

Trp Phe Arg Leu Lys Arg Asn Thr Asn  
290 295

<210> 32

<211> 285

<212> PRT

<213> Oryza sativa

<200>

<223> OSC5489.C1.p2.fg polypeptide

<400> 32

Met Ala Asp Ala Gly His Asp Glu Ser Gly Ser Pro Pro Arg Ser Gly  
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Gly Val Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg  
20 25 30

Ile Met Lys Lys Ala Val Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala  
35 40 45

Lys Glu Thr Leu Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr  
50 55 60

Ser Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Ile Asn  
65 70 75 80

Gly Glu Asp Leu Leu Phe Ala Met Gly Thr Leu Gly Phe Glu Glu Tyr  
85 90 95

Val Asp Pro Leu Lys Ile Tyr Leu His Lys Tyr Arg Glu Met Glu Gly

100

105

110

Asp Ser Lys Leu Ser Ser Lys Ala Gly Asp Gly Ser Val Lys Lys Asp  
115 120 125

Thr Ile Gly Pro His Ser Gly Ala Ser Ser Ser Ser Ala Gln Gly Met  
130 135 140

Val Gly Ala Tyr Thr Gln Gly Met Gly Tyr Met Gln Pro Gln Ser Asn  
145 150 155 160

Phe His Ile Leu Val Val Leu Gln Ser Phe Ala Phe Pro Tyr Met Tyr  
165 170 175

Gln Val Ala Gln Ile Tyr Cys Asn Lys Tyr Glu Val Ser Arg Glu Gln  
180 185 190

Ile Trp Asp Thr Pro Gln Ile Met Glu Leu Ser Pro Trp Ile Pro Tyr  
195 200 205

Thr Ile Asn Arg Ile Trp Lys Glu Thr His Gly Ser Gln Asp Ile Arg  
210 215 220

Ile Gln Gly Arg Pro Arg Glu Ala Ala Asn Ser Ala Leu Asp Trp Gln  
225 230 235 240

Trp Pro Ser Lys His Ser Ser Leu Ala Ser Asn Phe Tyr Gly Thr Arg  
245 250 255

Val Val Gly Gly His His Glu Tyr Gln Arg Ser Thr Lys Lys Asp Thr  
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Thr His Val Asn Phe Ala Ser Gly Leu Gly Asp Leu Gly  
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<213> Zea mays

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ctggggccatg accacgctcg gcttcgaggc ctacgtcgcc ccactcaagt cctacctcaa 420
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 <211> 174  
 <212> PRT  
 <213> Zea mays

<200>  
 <223> LIB3732-044-Q6-K6-C4 polypeptide

<400> 34

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Val Gly Ser Pro Leu Ser Asp Asn Glu Ser Gly Ala Ala Ala Ala Ala  
20 25 30

Gly Gly Gly Gly Cys Gly Ser Ser Val Gly Tyr Cys Gly Gly Gly Gly  
35 40 45

Gly Glu Ser Pro Ala Lys Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn  
50 55 60

Val Ser Arg Ile Met Lys Arg Ser Leu Pro Ala Asn Ala Lys Ile Ser  
65 70 75 80

Lys Glu Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser  
85 90 95

Phe Val Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys  
100 105 110

Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly Phe  
115 120 125

Glu Ala Tyr Val Ala Pro Leu Lys Ser Tyr Leu Asn Arg Tyr Arg Glu  
130 135 140

Ala Glu Gly Glu Lys Ala Ala Val Leu Gly Gly Gly Ala Arg His Gly  
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Asp Gly Gly Gly Ala Ala Asp Asp Ala Gly Pro Leu Ala Gly  
165 170

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<211> 1199  
<212> DNA  
<213> Zea mays

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<211> 166  
<212> PRT  
<213> Zea mays

<200>  
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<400> 36

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Val Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile  
20 25 30

Met Lys Lys Ala Val Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys  
35 40 45

Glu Thr Leu Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr Ser  
50 55 60

Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Ile Asn Gly  
65 70 75 80

Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu Glu Tyr Val  
85 90 95

Glu Pro Leu Lys Ile Tyr Leu Gln Lys Tyr Lys Glu Met Glu Gly Asp  
100 105 110

Ser Lys Leu Ser Thr Lys Ala Gly Glu Gly Ser Val Lys Lys Asp Ala  
115 120 125

Ile Ser Pro His Gly Gly Thr Ser Ser Ser Ser Asn Gln Leu Val Gln  
130 135 140

His Gly Val Tyr Asn Gln Gly Met Gly Tyr Met Gln Pro Gln Val Ile  
145 150 155 160

Tyr Arg Thr Val Ile Cys  
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<211> 564

<212> DNA

<213> Zea mays

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<223> ZEAMA-08NOV01-CLUSTER719\_10

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 <213> Zea mays

<220>  
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<400> 38

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 1 5 10 15

Ala Leu Pro Ala Arg Ser Leu Arg His Leu Arg Pro Pro Pro Ala Leu  
 20 25 30

Gly Arg Ser Pro Pro Ala Leu Pro Ser Leu His Val Ala Arg Ala Arg  
 35 40 45

Ala Tyr Ile Ser Ala Arg Gly Gly Ala His Gly Gly Arg Ser Gly Glu  
 50 55 60

Pro Trp Gly Arg Arg Arg Glu Pro His Ala Glu Arg Glu Pro Pro Gly  
 65 70 75 80

Pro Ala Glu Val Glu Ala Val Ala Ala Val Arg Glu Gln Asp Arg Phe  
 85 90 95

Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala Ile Pro Ala  
 100 105 110

Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val  
 115 120 125

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Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Asp Lys Cys Gln  
130 135 140

Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met  
145 150 155 160

Ala Thr Leu Gly Phe Glu Asp Tyr Ile Glu Pro Leu Lys Val Tyr Leu  
165 170 175

Gln Lys Tyr Arg Glu Met Glu Gly Asp Ser Lys Xaa  
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<200>  
<223> ZEAMA-08NOV01-CLUSTER719\_2

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 <212> PRT  
 <213> Zea mays

<200>  
 <223> ZEAMA-08NOV01-CLUSTER719\_2 polypeptide

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Val Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile  
 20 25 30

Met Lys Lys Ala Val Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys  
 35 40 45

Glu Thr Leu Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr Ser  
 50 55 60

Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Ile Asn Gly  
 65 70 75 80

Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu Glu Tyr Val  
 85 90 95

Glu Pro Leu Lys Ile Tyr Leu Gln Lys Tyr Lys Glu Met Glu Gly Asp  
 100 105 110

Ser Lys Leu Ser Thr Lys Ala Gly Glu Gly Ser Val Lys Lys Asp Ala  
 115 120 125

Ile Ser Pro His Gly Gly Thr Ser Ser Ser Ser Asn Gln Leu Val Gln  
 130 135 140

His Gly Val Tyr Asn Gln Gly Met Gly Tyr Met Gln Pro Gln Tyr His  
 145 150 155 160

Asn Gly Glu Thr

<210> 41  
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 <212> DNA  
 <213> Zea mays

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cctgctgtgg gccatggcca cgctgggggt tgaggactat attgaacccc tcaaggtgta      540
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<210> 42
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<212> PRT
<213> Zea mays

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Ser Gly Ser Pro Arg Gly Gly Gly Gly Gly Gly Ser Val Arg Glu Gln
20          25          30
Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala

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35

40

45

Ile Pro Ala Asn Gly Lys Thr Ile Pro Ala Asn Gly Lys Ile Ala Lys  
50 55 60

Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe  
65 70 75 80

Ile Thr Ser Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr  
85 90 95

Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu  
100 105 110

Asp Tyr Ile Glu Pro Leu Lys Val Tyr Leu Gln Lys Tyr Arg Glu Met  
115 120 125

Glu Gly Asp Ser Lys Leu Thr Ser Lys Ser Ser Asp Gly Ser Ile Lys  
130 135 140

Lys Asp Ala Leu Gly His Val Gly Ala Ser Ser Ser Ala Val Gln Gly  
145 150 155 160

Met Gly Gln Gln Gly Thr Tyr Asn Gln Gly Met Gly Tyr Met Gln Pro  
165 170 175

Gln Tyr His Asn Gly Asp Ile Ser Asn  
180 185

<210> 43  
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agttcatctc cttcatcact agcgaagcga gtgacaagtg ccagaggagg aagcggaaga 360  
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ctgtgtacta ctccagtaaa tacagctagt aaacacatta tttttataag gtgaaccaat	720
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 <212> PRT

<213> Zea mays

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20 25 30

Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala  
35 40 45

Ile Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu Thr Val Gln  
50 55 60

Glu Cys Val Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Asp  
65 70 75 80

Lys Cys Gln Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu  
85 90 95

Trp Ala Met Ala Thr Leu Gly Phe Glu Asp Tyr Ile Glu Pro Leu Lys  
100 105 110

Val Tyr Leu Gln Lys Tyr Arg Glu Val Arg Thr Val Phe Gly Asn Leu  
115 120 125

Gly Val Arg Ser Cys Asn Arg Gln Ser Val Thr Trp Pro Ile Val Pro  
130 135 140

Leu Ile Glu Leu Lys  
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<210> 45

<211> 1255

<212> DNA

<213> Zea mays

<200>

<223> ZEAMA-08NOV01-CLUSTER719\_5

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<400> 46

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Ser Gly Ser Pro Arg Gly Gly Gly Gly Gly Gly Ser Val Arg Glu Gln  
20 25 30

Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala  
35 40 45

Ile Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu Thr Val Gln  
50 55 60



MBI-0022CIP.ST25.txt

Glu Cys Val Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Asp  
65 70 75 80

Lys Cys Gln Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu  
85 90 95

Trp Ala Met Ala Thr Leu Gly Phe Glu Asp Tyr Ile Glu Pro Leu Lys  
100 105 110

Val Tyr Leu Gln Lys Tyr Arg Glu Met Glu Gly Asp Ser Lys Leu Thr  
115 120 125

Ala Lys Ser Ser Asp Gly Ser Ile Lys Lys Asp Ala Leu Gly His Val  
130 135 140

Gly Ala Ser Ser Ser Ala Ala Gln Gly Met Gly Gln Gln Gly Ala Tyr  
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Asn Gln Gly Met Gly Tyr Met Gln Pro Gln Tyr His Asn Gly Asp Ile  
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Ser Asn

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gactcgccaa atttccctcc ctctcctag ccttctcgtc gctcctgttc ttctcgcatc 180  
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gggcgagctg tcgtcgccgc gggagcagga ccggttctctg cccatcgcca acgtgagccg 360  
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gcgcgagaag cgcaagacca tcaacggcga cgacctgctg tgggcatga ccacgctcgg 540  
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cggcattgat atgatgatga tggggcagcc catgtacggc ggctcgcagc cgcagcaaca      780
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ctgcctgtcc ttgtacgttt actaattatt gctgcctgta tgtaaataaa aatctgaggg    1080
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<210> 48  
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 <212> PRT  
 <213> Zea mays

<200>  
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<400> 48

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Glu Leu Ser Ser Pro Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn  
                  20                   25                   30

Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile Ser  
                  35                   40                   45

Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser  
                  50                   55                   60

Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys  
                  65                   70                   75                   80

Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly Phe  
                  85                   90                   95

Glu Asp Tyr Val Glu Pro Leu Lys His Tyr Leu His Lys Phe Arg Glu  
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Ile Glu Gly Glu Arg Ala Ala Ala Ser Ala Gly Ala Ser Gly Ser Gln  
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Gln Gln Gln Gln Gln Gly Glu Leu Pro Arg Gly Ala Ala Asn Ala Ala  
130 135 140

Gly Tyr Ala Gly Tyr Gly Ala Pro Gly Ser Gly Gly Met Met Met Met  
145 150 155 160

Met Met Gly Gln Pro Met Tyr Gly Gly Ser Gln Pro Gln Gln Gln Pro  
165 170 175

Pro Gln Pro Gln Pro Pro Gln Gln Gln Gln Gln Gln His Gln Gln His  
180 185 190

His Met Ala Met Gly Gly Arg Gly Gly Phe Gly Gln Gln Gly Gly Gly  
195 200 205

Gly Gly Ser Ser Ser Ser Ser Gly Leu Gly Arg Gln Asp Arg Ala  
210 215 220

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<211> 1064  
<212> DNA  
<213> Zea mays

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<223> G3436 ZEAMA-08NOV01-CLUSTER90408\_2

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gttcggtggc tcggccgcga tgccggactc cgacaacgag tccggcgggc cgagcaacgc 180  
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cggcgcgggc gggggaagcg gtatgatcat gatgatgggg cagcccatgt acggcggtc 660  
ccgcgcggcc gcgtcgtccg ggtcgtaccc gcaccaccag atggccatgg gcggaaaagg 720  
tggcgccctat ggctacggcg gaggctcgtc gtcgtcgccc tcagggctcg gcaggtagga 780  
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 atggttaaga tagctccata acctctcggt aattaatcct gtgatttgta ctcccaagct 1020  
 gctgctaaac tgagctatga cacaatacaa atgctgccat taac 1064

<210> 50  
 <211> 212  
 <212> PRT  
 <213> Zea mays

<200>  
 <223> G3436 ZEAMA-08NOV01-CLUSTER90408\_2 polypeptide  
 <400> 50

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 1 5 10 15

Ser Ser Pro Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Val Ser  
 20 25 30

Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile Ser Lys Asp  
 35 40 45

Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile  
 50 55 60

Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr Ile  
 65 70 75 80

Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly Phe Glu Asp  
 85 90 95

Tyr Val Glu Pro Leu Lys Leu Tyr Leu His Lys Phe Arg Glu Leu Glu  
 100 105 110

Gly Glu Lys Ala Ala Thr Thr Ser Ala Ser Ser Gly Pro Gln Pro Pro  
 115 120 125

Leu His Arg Glu Thr Thr Pro Ser Ser Ser Thr His Asn Gly Ala Gly  
 130 135 140

Gly Pro Val Gly Gly Tyr Gly Met Tyr Gly Gly Ala Gly Gly Gly Ser  
 145 150 155 160

Gly Met Ile Met Met Met Gly Gln Pro Met Tyr Gly Gly Ser Pro Pro  
 165 170 175

MBI-0022CIP.ST25.txt

Ala Ala Ser Ser Gly Ser Tyr Pro His His Gln Met Ala Met Gly Gly  
180 185 190

Lys Gly Gly Ala Tyr Gly Tyr Gly Gly Gly Ser Ser Ser Ser Pro Ser  
195 200 205

Gly Leu Gly Arg  
210

<210> 51  
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<212> DNA  
<213> Glycine max

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<223> G3473 GLYMA-28NOV01-CLUSTER33504\_4

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<211> 170  
<212> PRT  
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Gly Ser Glu Met Ser Pro Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala  
20 25 30

Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile  
35 40 45

Ser Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile  
50 55 60

Ser Phe His Ser Pro Gly Gly Leu Ala Gly Glu Cys Gln Lys Glu Lys  
65 70 75 80

Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu  
85 90 95

Gly Phe Glu Glu Tyr Val Glu Pro Leu Lys Val Tyr Leu His Lys Tyr  
100 105 110

Arg Glu Leu Glu Gly Glu Lys Thr Ala Met Met Gly Arg Pro His Glu

115

120

125

Arg Asp Glu Gly Tyr Gly His Ala Thr Pro Met Met Ile Met Met Gly  
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His Gln Gln Gln Gln His Gln Gly His Val Tyr Gly Ser Gly Thr Thr  
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Thr Gly Ser Ala Ser Ser Ala Arg Thr Arg  
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<212> DNA  
<213> Oryza sativa

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<212> PRT  
<213> Oryza sativa

<200>

<223> ORYSA-22JAN02-CLUSTER119015\_1 polypeptide

<400> 54

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Gly Val Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg  
20 25 30

Ile Met Lys Lys Ala Val Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala  
35 40 45

Lys Glu Thr Leu Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr  
50 55 60

Ser Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Ile Asn  
65 70 75 80

Gly Glu Asp Leu Leu Phe Ala Met Gly Thr Leu Gly Phe Glu Glu Tyr  
85 90 95

Val Asp Pro Leu Lys Ile Tyr Leu His Lys Tyr Arg Glu Met Glu Gly  
100 105 110

Asp Ser Lys Leu Ser Ser Lys Ala Gly Asp Gly Ser Val Lys Lys Asp  
115 120 125

Thr Ile Gly Pro His Ser Gly Ala Ser Ser Ser Ser Ala Gln Gly Met  
130 135 140

Val Gly Ala Tyr Thr Gln Gly Met Gly Tyr Met Gln Pro Gln Tyr His  
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Asn Gly Asp Thr

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<211> 870

<212> DNA

<213> Zea mays

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<400> 55

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cggcgggagc cacgagagcg ggagccccag gggagggcgga ggcggtggca gcgtcagggg 120



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 <400> 56

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Gly Gly Ser His Glu Ser Gly Ser Pro Arg Gly Gly Gly Gly Gly Gly  
 20 25 30

Ser Val Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg  
 35 40 45

Ile Met Lys Lys Ala Ile Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala  
 50 55 60

Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile Thr  
 65 70 75 80

Ser Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr Ile Asn  
 85 90 95

Gly Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu Asp Tyr

100 105 110

Ile Glu Pro Leu Lys Val Tyr Leu Gln Lys Tyr Arg Glu Met Glu Gly  
115 120 125

Asp Ser Lys Leu Thr Ala Lys Ser Ser Asp Gly Ser Ile Lys Lys Asp  
130 135 140

Ala Leu Gly His Val Gly Ala Ser Ser Ser Ala Ala Glu Gly Met Gly  
145 150 155 160

Gln Gln Gly Ala Tyr Asn Gln Gly Met Gly Tyr Met Gln Pro Gln Tyr  
165 170 175

His Asn Gly Asp Ile Ser Asn  
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<223> Xaa can be any naturally occurring amino acid

<200>  
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<400> 58

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Met Lys Lys Ala Val Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys  
20 25 30

Glu Thr Leu Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr Ser  
35 40 45

Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Ile Asn Gly  
50 55 60

Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu Glu Tyr Val  
65 70 75 80

Glu Pro Leu Lys Ile Tyr Leu Gln Lys Tyr Lys Glu Met Glu Gly Asp  
85 90 95

Ser Lys Leu Ser Thr Lys Ala Gly Glu Gly Ser Val Lys Lys Asp Ala  
100 105 110

Ile Ser Pro His Gly Gly Thr Ser Ser Ser Ser Asn Gln Leu Val Gln  
115 120 125

His Gly Val Tyr Asn Gln Gly Met Gly Tyr Met Gln Pro Gln Tyr His  
130 135 140

Asn Gly Glu Thr  
145

<210> 59  
<211> 720  
<212> DNA

<213> Triticum aestivum

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<222> (2)..(2)

<223> n is a, c, g, or t

<220>

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<223> n is a, c, g, or t

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<222> (690)..(690)

<223> n is a, c, g, or t

<200>

<223> Ta\_S45374

<400> 59

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gaattcggca ccagccacca ccttccctcc ctccacgagc ccgtctatat aaggaggagg	180
gccggatgtc ggacgcgccc gcgagcccc cgggcggcgg cggcggcgga ggaggcggcg	240
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ccaaggagcg caaggagacc gtgcaggagt gcgtctccga gttcatctcc ttcacacca	420
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<210> 60

<211> 179

<212> PRT

<213> Triticum aestivum

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<223> Xaa can be any naturally occurring amino acid

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<400> 60

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 1 5 10 15

Gly Gly Gly Ser Asp Asp Gly Gly Gly Gly Gly Gly Phe Gly Gly Val  
 20 25 30

Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met  
 35 40 45

Lys Lys Ala Ile Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu  
 50 55 60

Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu  
 65 70 75 80

Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp  
 85 90 95

Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu Glu Tyr Ile Glu  
 100 105 110

Pro Leu Lys Val Tyr Leu Gln Lys Tyr Arg Glu Thr Glu Gly Asp Ser  
 115 120 125

Lys Leu Ala Gly Lys Ser Gly Glu Val Ser Val Lys Lys Asp Ala Leu  
 130 135 140

Gly Pro His Gly Gly Ala Ser Gly Thr Ser Ala Gln Gly Met Gly Gln  
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Gln Val His Thr Ile Gln Glu Trp Xaa Ile Cys Asn Leu Ser Thr Ile  
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ctctgggcca tgaccacctt cggttcgag gactatgtcg acccgctcaa gcactacctn	360
cacaagttcc gcgagatcga gggcnagagg gccgcgcgcca catcaacatc aaccacgccc	420
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gatgatgatg gggcagccca tgtaccggtt ngccggccgc accacaagga gcangnacc	540
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gggtctctcg natcctnnng ggttttgacc gaaaaaanng ganacctttt cctttttctt	660
ttcttttctt tttggannct gaccnnaagg ggaggggntt ttcaaacttn tgttncttct	720
ttttgggtga aaaccctnct tgtnanctta aaattctttt cnnccccagg ggnggggaan	780
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Ser Pro Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Val Ser Arg  
 35 40 45

Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile Ser Lys Asp Ala  
 50 55 60

Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile Thr  
 65 70 75 80

Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr Xaa Asn  
 85 90 95

Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly Phe Glu Asp Tyr  
 100 105 110

Val Asp Pro Leu Lys His Tyr Xaa His Lys Phe Arg Glu Ile Glu Gly  
 115 120 125

Xaa Arg Ala Ala Ala Thr Ser Thr Ser Thr Thr Pro Asp Met Pro Arg  
 130 135 140

Asn Asn Asn Asn Asn Ala Arg Arg Leu Pro Arg Arg Pro Gly Arg His  
 145 150 155 160

Asp Asp Asp Gly Ala Ala His Val Pro Val Xaa Arg Pro His His Lys  
 165 170 175

Glu Xaa Xaa Pro Asn Xaa Lys Ile Ala Met Gly Arg Gly Glu Ala Gly  
 180 185 190

Phe Xaa Tyr Phe Gly Gly Gly Xaa Gly Xaa Ser Xaa Ser Xaa Xaa Val  
 195 200 205

Leu Thr Glu Lys Xaa Gly Xaa Leu Phe Leu Phe Leu Phe Phe Ser Phe

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210                                     215                                     220

Trp Xaa Leu Thr Xaa Arg Gly Gly Xaa Phe Gln Thr Xaa Val Xaa Ser
225                                     230                                     235                                     240

Phe Trp Val Lys Thr Xaa Leu Xaa Xaa Leu Lys Phe Phe Xaa Xaa Pro
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Gly Xaa Gly Xaa Xaa Xaa Phe Phe Pro Xaa Val Xaa
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tcccttcttc tccaacgtcc gatcttccag ttccctccat cccagtatg gcggatggtc      180
aaggttcgtc taggtcaccg gcgagtccaa acggaggtgg tagtcatgag agtgggtggg      240
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gagaagacgg gtggagttga aaacatatta tatatataga tggttcttct gctgtaacct      780
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20 25 30

Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile Met  
35 40 45

Lys Lys Ala Leu Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys Glu  
50 55 60

Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu  
65 70 75 80

Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr Ile Asn Gly Asp  
85 90 95

Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu Asp Tyr Ile Glu  
100 105 110

Pro Leu Lys Val Tyr Leu Ala Arg Tyr Arg Glu Met Glu Gly Thr Ser  
115 120 125

Lys Ala Ala Asp Gly Ser Thr Lys Arg Asp Gly Met Gln Pro Gly Pro  
130 135 140

Asn Ser Gln Leu Ala His Gln Gly Ser Tyr Ser Gln Gly Met Asn Tyr  
145 150 155 160

Gly Asn Ser Gln Gly Gln His Met Met Val Pro Met Gln Gly Thr Glu  
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Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile Ser  
 35 40 45

Lys Asp Ala Lys Glu Val Val Gln Glu Cys Val Ser Glu Phe Ile Ser  
 50 55 60

Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys  
 65 70 75 80

Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly Phe

Glu Glu Tyr Ile Glu Pro Leu Lys Ile Tyr Leu Gln Arg Phe Arg Asp  
100 105 110

Leu Glu Gly Gln Lys Ser Gly Val Ser Gly Glu Lys Asp His Ser Gly  
115 120 125

Ser Val Gly Tyr Val Glu Asp Tyr His Gly Met Met Met Met Gly Ser  
130 135 140

Gln His His Gln Gly Arg Gly Tyr Gly Thr Gly Val Tyr Asn His His  
145 150 155 160

Thr Gly Glu Asn Ala Ala Gly Val Gly Thr Gly Gly Ser Arg Phe Pro  
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Asp Val Gly Arg Gln Arg  
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aagaagatca tgaaggctga tccagatgtg cacatgggtct ccgcagaggg tccgatcatc 240  
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ccgggagtgg tgatgggaac tcctatgggt ggtagtggaa tgtacgcgcc atcgaggcg 540  
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Asn Pro Gln Leu Arg Asn Tyr Trp Ile Glu Gln Met Glu Thr Val Ser  
35 40 45

Asp Phe Lys Asn Arg Gln Leu Pro Leu Ala Arg Ile Lys Lys Ile Met  
50 55 60

Lys Ala Asp Pro Asp Val His Met Val Ser Ala Glu Ala Pro Ile Ile  
65 70 75 80

Phe Ala Lys Ala Cys Glu Met Phe Ile Val Asp Leu Thr Met Arg Ser  
85 90 95

Trp Leu Lys Ala Glu Glu Asn Lys Arg His Thr Leu Gln Lys Ser Asp  
100 105 110

Ile Ser Asn Ala Val Ala Ser Ser Phe Thr Tyr Asp Phe Leu Leu Asp  
115 120 125

Val Val Pro Lys Asp Glu Ser Ile Ala Thr Ala Asp Pro Gly Phe Val  
130 135 140

Ala Met Pro His Pro Asp Gly Gly Gly Val Pro Gln Tyr Tyr Tyr Pro  
145 150 155 160

Pro Gly Val Val Met Gly Thr Pro Met Val Gly Ser Gly Met Tyr Ala  
165 170 175

Pro Ser Gln Ala Trp Pro Ala Ala Ala Gly Asp Gly Glu Asp Asp Ala  
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Glu Asp Asn Gly Gly Asn Gly Gly Gly Asn  
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Gly Leu Val Val Val Val Glu Asp Gln Gln Gln Glu Glu Ser Met Met
35          40          45

Val Lys Glu Gln Asp Arg Leu Leu Pro Ile Ala Asn Val Gly Arg Ile
50          55          60

Met Lys Asn Ile Leu Pro Ala Asn Ala Lys Val Ser Lys Glu Ala Lys
65          70          75          80

Glu Thr Met Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr Gly
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Glu Ala Ser Asp Lys Cys His Lys Glu Lys Arg Lys Thr Val Asn Gly
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Ala Gln Leu Lys Lys Tyr Leu His Arg Tyr Arg Val Leu Glu Gly Glu  
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ccaggaagcc cttcttcaaa gaccaacaac aacaacaaca acaacaaaga acaagaccgg 180  
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actggtgaag cttctgacaa gtgtcaaaga gaaaagagga agaccatcaa tggagatgat 360  
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gacaaaaaca ataacaacat gtcatgtact agttacatct ctcatcatca tccttctcca 600  
ttcctaccag tggatcatca accttttccc aatattgctt tctctcctaa atcattgcag 660  
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Glu Thr Asn Pro Gly Ser Pro Ser Ser Lys Thr Asn Asn Asn Asn Asn  
20 25 30

Asn Asn Lys Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Val Gly Arg  
35 40 45

Ile Met Lys Lys Val Leu Pro Gly Asn Gly Lys Ile Ser Lys Asp Ala  
50 55 60

Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr  
65 70 75 80

Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr Ile Asn  
85 90 95

Gly Asp Asp Ile Ile Trp Ala Ile Thr Thr Leu Gly Phe Glu Asp Tyr  
100 105 110

Val Ala Pro Leu Lys Val Tyr Leu Cys Lys Tyr Arg Asp Thr Glu Gly  
115 120 125

Glu Lys Val Asn Ser Pro Lys Gln Gln Gln Gln Arg Gln Gln Gln Gln  
130 135 140

Gln Ile Gln Gln Gln Asn His His Asn Tyr Gln Phe Gln Glu Gln Asp  
145 150 155 160

Gln Asn Asn Asn Asn Met Ser Cys Thr Ser Tyr Ile Ser His His His  
165 170 175

Pro Ser Pro Phe Leu Pro Val Asp His Gln Pro Phe Pro Asn Ile Ala  
180 185 190

Phe Ser Pro Lys Ser Leu Gln Lys Gln Phe Pro Gln Gln His Asp Asn  
195 200 205

Asn Ile Asp Ser Ile His Trp  
210 215

<210> 73  
<211> 610  
<212> DNA  
<213> Oryza sativa

<200>  
<223> G3395

<400> 73

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agaccctgca ggagtgcgtc tcggagttca tctccttcgt caccagcgag gcgagcgaca 240
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<210> 74  
 <211> 164  
 <212> PRT  
 <213> Oryza sativa

<200>  
 <223> G3395 polypeptide

<400> 74

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Gly Val Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg  
20 25 30

Ile Met Lys Lys Ala Val Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala  
35 40 45

Lys Glu Thr Leu Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr  
50 55 60

Ser Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Ile Asn  
65 70 75 80

Gly Glu Asp Leu Leu Phe Ala Met Gly Thr Leu Gly Phe Glu Glu Tyr  
85 90 95

Val Asp Pro Leu Lys Ile Tyr Leu His Lys Tyr Arg Glu Met Glu Gly  
100 105 110

Asp Ser Lys Leu Ser Ser Lys Ala Gly Asp Gly Ser Val Lys Lys Asp

115

120

125

Thr Ile Gly Pro His Ser Gly Ala Ser Ser Ser Ser Ala Gln Gly Met  
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Val Gly Ala Tyr Thr Gln Gly Met Gly Tyr Met Gln Pro Gln Tyr His  
145 150 155 160

Asn Gly Asp Thr

<210> 75  
<211> 761  
<212> DNA  
<213> Oryza sativa

<200>  
<223> G3398 AP005193

<400> 75  
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<210> 76  
<211> 224  
<212> PRT  
<213> Oryza sativa

<200>  
<223> G3398 AP005193 polypeptide

<400> 76

Met Pro Asp Ser Asp Asn Glu Ser Gly Gly Pro Ser Asn Ala Gly Glu

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      20              25              30
Ser Arg Ile Met Lys Arg Ala Leu Pro Ala Asn Ala Lys Ile Ser Lys
      35              40              45
Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe
      50              55              60
Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr
      65              70              75              80
Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly Phe Glu
      85              90              95
Asp Tyr Ile Asp Pro Leu Lys Leu Tyr Leu His Lys Phe Arg Glu Leu
      100             105             110
Glu Gly Glu Lys Ala Ile Gly Ala Ala Gly Ser Gly Gly Gly Gly Ala
      115             120             125
Ala Ser Ser Gly Gly Ser Gly Ser Gly Ser Gly Ser His His His Gln
      130             135             140
Asp Ala Ser Arg Asn Asn Gly Gly Tyr Gly Met Tyr Gly Gly Gly Gly
      145             150             155             160
Gly Met Ile Met Met Met Gly Gln Pro Met Tyr Gly Ser Pro Pro Ala
      165             170             175
Ser Ser Ala Gly Tyr Ala Gln Pro Pro Pro Pro His His His His His
      180             185             190
Gln Met Val Met Gly Gly Lys Gly Ala Tyr Gly His Gly Gly Gly Gly
      195             200             205
Gly Gly Gly Pro Ser Pro Ser Ser Gly Tyr Gly Arg Gln Asp Arg Leu
      210             215             220

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 <213> Zea mays

<200>  
 <223> G3434

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aggagtacgt cgagcctctc aagatttacc tacaaaagta caaagagatg gagggtgata      420
gcaagctgtc tacaaaggct ggcgagggct ctgtaaagaa ggatgcaatt agtccccatg      480
gtggcaccag tagctcaagt aatcagttgg ttcagcatgg agtctacaac caagggatgg      540
gctatatgca gccacagtac cacaatgggg aaacctata aagggttaat acagcagcaa      600
tttatgctag ggaagtctct gcattgctta ccatgtgtat tggcagaaaa caggaggcac      660
ttacaaaggg tgtaaatctc tgcgatggct gcctctcagg tgtaaattgg cttcggttta      720
gcgctgcttt tgtccgtata tttaggatga tttgactggt gctacttttg gcaacctttt      780
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tggtgattaa aaaaaa                                     856

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<210> 78
<211> 164
<212> PRT
<213> Zea mays

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<200>
<223> G3434 polypeptide

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<400> 78

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Met Ala Asp Asp Gly Gly Ser His Glu Gly Ser Gly Gly Gly Gly Gly
1           5           10          15

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```

Val Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile Ser Arg Ile
          20          25          30

```

```

Met Lys Lys Ala Val Pro Ala Asn Gly Lys Ile Ala Lys Asp Ala Lys
          35          40          45

```

```

Glu Thr Leu Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Val Thr Ser
          50          55          60

```

```

Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Ile Asn Gly
          65          70          75          80

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Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu Glu Tyr Val  
85 90 95

Glu Pro Leu Lys Ile Tyr Leu Gln Lys Tyr Lys Glu Met Glu Gly Asp  
100 105 110

Ser Lys Leu Ser Thr Lys Ala Gly Glu Gly Ser Val Lys Lys Asp Ala  
115 120 125

Ile Ser Pro His Gly Gly Thr Ser Ser Ser Ser Asn Gln Leu Val Gln  
130 135 140

His Gly Val Tyr Asn Gln Gly Met Gly Tyr Met Gln Pro Gln Tyr His  
145 150 155 160

Asn Gly Glu Thr

<210> 79  
<211> 772  
<212> DNA  
<213> Glycine max

<200>  
<223> G3472

<400> 79  
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tattaattga ttactataag gatggtgata ttgatttat attctgttg attttagaaa 660  
cacacccgct ccagcttgta attgttgctt gaaacttcgt tgttgagaga atatagacat 720  
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<211> 171  
<212> PRT  
<213> Glycine max

<200>  
<223> G3472 polypeptide

<400> 80

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1 5 10 15

Gly Ser Asn Glu Phe Ser Gly Cys Arg Glu Gln Asp Arg Phe Leu Pro  
20 25 30

Ile Ala Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala  
35 40 45

Lys Ile Ser Lys Glu Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu  
50 55 60

Phe Ile Ser Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Lys Glu  
65 70 75 80

Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr  
85 90 95

Leu Gly Phe Glu Glu Tyr Val Glu Pro Leu Lys Val Tyr Leu His Lys  
100 105 110

Tyr Arg Glu Leu Glu Gly Glu Lys Thr Ala Met Met Gly Arg Pro His  
115 120 125

Glu Arg Asp Glu Gly Tyr Gly His Ala Thr Pro Met Met Ile Met Met  
130 135 140

Gly His Gln Gln Gln Gln His Gln Gly His Val Tyr Gly Ser Gly Thr  
145 150 155 160

Thr Thr Gly Ser Ala Ser Ser Ala Arg Thr Arg  
165 170

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<212> DNA  
<213> Glycine max

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<223> G3474

<400> 81

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gctatgatgg gaaggccaca tgagagggat gagggttatg gccatggcca tggatcatgca      480
actcctatga tgacgatgat gatggggcat cagccccagc accagcacca gcaccagcac      540
cagcaccagc accagggaca cgtgtatgga tctggatcag catcttctgc aagaactaga      600
tagcatgtgt catctgttta agcttaattg attttattat gaggatgata tgatataaga      660
tttatattcg tatatgtttg gttttagaaa tacaccagct ccagcttgta attgcttgaa      720
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 <212> PRT  
 <213> Glycine max

<200>  
 <223> G3474 polypeptide  
 <400> 82

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Gly Ser Asn Glu Leu Ser Gly Cys Arg Glu Gln Asp Arg Phe Leu Pro  
 20 25 30

Ile Ala Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala  
 35 40 45

Lys Ile Ser Lys Glu Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu  
 50 55 60

Phe Ile Ser Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Lys Glu

65		70		75		80									
Lys	Arg	Lys	Thr	Ile	Asn	Gly	Asp	Asp	Leu	Leu	Trp	Ala	Met	Thr	Thr
				85					90					95	
Leu	Gly	Phe	Glu	Asp	Tyr	Val	Asp	Pro	Leu	Lys	Ile	Tyr	Leu	His	Lys
			100					105					110		
Tyr	Arg	Glu	Met	Glu	Gly	Glu	Lys	Thr	Ala	Met	Met	Gly	Arg	Pro	His
		115					120					125			
Glu	Arg	Asp	Glu	Gly	Tyr	Gly	His	Gly	His	Gly	His	Ala	Thr	Pro	Met
		130				135					140				
Met	Thr	Met	Met	Met	Gly	His	Gln	Pro	Gln	His	Gln	His	Gln	His	Gln
145					150				155						160
His	Gln	His	Gln	His	Gln	Gly	His	Val	Tyr	Gly	Ser	Gly	Ser	Ala	Ser
				165					170					175	
Ser	Ala	Arg	Thr	Arg											
			180												

<210> 83  
 <211> 967  
 <212> DNA  
 <213> Glycine max

<200>  
 <223> G3477

<400> 83	
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gtaccttccc attgccaaca tcagccgcat catgaagaag gctctgcctc ccaatggcaa	300
gattgcgaag gatgcaaaaag acacaatgca agaatgcgtt tctgaattca tcagcttcat	360
taccagcgag gcgagtgaga aatgccagaa ggagaagaga aagacaatca atggagacga	420
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<210> 84  
 <211> 174  
 <212> PRT  
 <213> Glycine max

<200>  
 <223> G3477 polypeptide

<400> 84

Met Ser Asp Ala Pro Ala Ser Pro Ser His Glu Ser Gly Gly Glu Gln  
 1 5 10 15

Ser Pro Arg Gly Ser Leu Ser Gly Ala Ala Arg Glu Gln Asp Arg Tyr  
 20 25 30

Leu Pro Ile Ala Asn Ile Ser Arg Ile Met Lys Lys Ala Leu Pro Pro  
 35 40 45

Asn Gly Lys Ile Ala Lys Asp Ala Lys Asp Thr Met Gln Glu Cys Val  
 50 55 60

Ser Glu Phe Ile Ser Phe Ile Thr Ser Glu Ala Ser Glu Lys Cys Gln  
 65 70 75 80

Lys Glu Lys Arg Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met  
 85 90 95

Ala Thr Leu Gly Phe Glu Asp Tyr Ile Glu Pro Leu Lys Val Tyr Leu  
 100 105 110

Ala Arg Tyr Arg Glu Ala Glu Gly Asp Thr Lys Gly Ser Ala Arg Ser  
 115 120 125

Gly Asp Gly Ser Ala Thr Pro Asp Gln Val Gly Leu Ala Gly Gln Asn  
 130 135 140

Ser Gln Leu Val His Gln Gly Ser Leu Asn Tyr Ile Gly Leu Gln Val  
 145 150 155 160

MBI-0022CIP.ST25.txt

Gln Pro Gln His Leu Val Met Pro Ser Met Gln Ser His Glu  
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<210> 85  
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<212> DNA  
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<200>  
<223> G3478

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<210> 86  
<211> 191  
<212> PRT  
<213> Glycine max

<200>  
<223> G3478 polypeptide

<400> 86

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Gly Ser Glu Met Ser Pro Arg Glu Gln Asp Arg Phe Leu Pro Ile Ala  
20 25 30

MBI-0022CIP.ST25.txt

Asn Val Ser Arg Ile Met Lys Lys Ala Leu Pro Ala Asn Ala Lys Ile  
35 40 45

Ser Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile  
50 55 60

Ser Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg  
65 70 75 80

Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly  
85 90 95

Phe Glu Asp Tyr Val Glu Pro Leu Lys Gly Tyr Leu Gln Arg Phe Arg  
100 105 110

Glu Met Glu Gly Glu Lys Thr Val Ala Ala Arg Asp Lys Asp Ala Pro  
115 120 125

Pro Leu Thr Asn Ala Thr Asn Ser Ala Tyr Glu Ser Ala Asn Tyr Ala  
130 135 140

Ala Ala Ala Ala Val Pro Gly Gly Ile Met Met His Gln Gly His Val  
145 150 155 160

Tyr Gly Ser Ala Gly Phe His Gln Val Ala Gly Gly Ala Ile Lys Gly  
165 170 175

Gly Pro Ala Tyr Pro Gly Pro Gly Ser Asn Ala Gly Arg Pro Arg  
180 185 190

<210> 87  
<211> 1231  
<212> DNA  
<213> Oryza sativa

<200>  
<223> G3394 Cl26105\_1

<400> 87  
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<210> 88  
 <211> 185  
 <212> PRT  
 <213> Oryza sativa

<200>  
 <223> G3394 C126105\_1 polypeptide

<400> 88

Met Ala Asp Gly Pro Gly Ser Pro Gly Gly Gly Gly Gly Ser His Glu  
 1 5 10 15

Ser Gly Ser Pro Arg Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly  
 20 25 30

Gly Gly Pro Leu Val Arg Gln Asp Arg Phe Leu Pro Ile Ala Asn Ile  
 35 40 45

Ser Arg Ile Met Lys Lys Ala Ile Pro Ala Asn Gly Lys Ile Ala Lys  
 50 55 60

Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe  
 65 70 75 80

Ile Thr Ser Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys Thr



85

90

95

Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu  
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Asp Tyr Ile Glu Pro Leu Lys Val Tyr Leu Gln Lys Tyr Arg Glu Met  
115 120 125

Glu Gly Asp Ser Lys Leu Thr Ala Lys Ala Gly Asp Gly Ser Val Lys  
130 135 140

Lys Asp Val Leu Gly Ser His Gly Gly Ser Ser Ser Ser Ala Gln Gly  
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Gln Tyr His Asn Gly Asp Val Ser Asn  
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<400> 90

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20 25 30

Gly Arg Ile Met Arg Arg Ala Val Pro Glu Asn Gly Lys Ile Ala Lys  
35 40 45

Asp Ser Lys Glu Ser Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe  
50 55 60

Ile Thr Ser Glu Ala Ser Asp Lys Cys Leu Lys Glu Lys Arg Lys Thr  
65 70 75 80

Ile Asn Gly Asp Asp Leu Ile Trp Ser Met Gly Thr Leu Gly Phe Glu  
85 90 95

Asp Tyr Val Glu Pro Leu Lys Leu Tyr Leu Arg Leu Tyr Arg Glu Thr  
100 105 110

Glu Gly Asp Thr Lys Gly Ser Arg Ala Ser Glu Leu Pro Val Lys Lys  
115 120 125

Asp Val Val Leu Asn Gly Asp Pro Gly Ser Ser Phe Glu Gly Met  
130 135 140

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20 25 30

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35 40 45

Ser Lys Asp Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile  
50 55 60

Ser Phe Ile Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg  
65 70 75 80

Lys Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly  
85 90 95

Phe Glu Asp Tyr Val Asp Pro Leu Lys His Tyr Leu His Lys Phe Arg  
100 105 110

Glu Ile Glu Gly Glu Arg Ala Ala Ala Ser Thr Thr Gly Ala Gly Thr  
115 120 125

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Ser Ala Ala Ser Thr Thr Pro Pro Gln Gln Gln His Thr Ala Asn Ala  
130 135 140

Ala Gly Gly Tyr Ala Gly Tyr Ala Ala Pro Gly Ala Gly Pro Gly Gly  
145 150 155 160

Met Met Met Met Met Gly Gln Pro Met Tyr Gly Ser Pro Pro Pro Pro  
165 170 175

Pro Gln Gln Gln Gln Gln Gln His His His Met Ala Met Gly Gly Arg  
180 185 190

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195 200 205

Ser Ser Gly His Gly Arg Gln Asn Arg Gly Ala  
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gtaagctatc tcttagagtt cagagcaggg caagaatctt gcaatgctca catgaacata 180  
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Gly Gly Gly Gly Cys Gly Ser Ser Val Gly Tyr Cys Gly Gly Gly Gly  
 35 40 45

Gly Glu Ser Pro Ala Lys Glu Gln Asp Arg Phe Leu Pro Ile Ala Asn  
 50 55 60

Val Ser Arg Ile Met Lys Arg Ser Leu Pro Ala Asn Ala Lys Ile Ser  
 65 70 75 80

Lys Glu Ala Lys Glu Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser  
 85 90 95

Phe Val Thr Gly Glu Ala Ser Asp Lys Cys Gln Arg Glu Lys Arg Lys  
 100 105 110

Thr Ile Asn Gly Asp Asp Leu Leu Trp Ala Met Thr Thr Leu Gly Phe  
 115 120 125

Glu Ala Tyr Val Ala Pro Leu Lys Ser Tyr Leu Asn Arg Tyr Arg Glu

130 135 140

Ala Glu Gly Glu Lys Ala Ala Val Leu Gly Gly Gly Ala Arg His Gly  
145 150 155 160

Asp Gly Ala Ala Arg Arg Thr Thr Pro Ala His Ser Pro Arg Asn Gly  
165 170 175

Ala Gly Gly Pro Val Gly Gly Tyr Gly Met Tyr Gly Gly Ala Gly Gly  
180 185 190

Gly Ser Gly Met Ile Met Met Met Gly Gln Pro Met Tyr Gly Gly Ser  
195 200 205

Pro Pro Ala Ala Ser Ser Gly Ser Tyr Pro His His Gln Met Ala Met  
210 215 220

Gly Gly Lys Gly Gly Ala Tyr Gly Tyr Gly Gly Gly Ser Ser Ser Ser  
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Pro Ser Gly Leu Gly Arg  
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<213> Arabidopsis thaliana

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<400> 96

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			20					25					30		

Lys	Pro	Ala	Gly	Arg	Lys	Lys	Phe	Arg	Glu	Thr	Arg	His	Pro	Ile	Tyr
		35					40					45			

Arg	Gly	Val	Arg	Gln	Arg	Asn	Ser	Gly	Lys	Trp	Val	Ser	Glu	Val	Arg
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Glu	Pro	Asn	Lys	Lys	Thr	Arg	Ile	Trp	Leu	Gly	Thr	Phe	Gln	Thr	Ala
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Glu	Met	Ala	Ala	Arg	Ala	His	Asp	Val	Ala	Ala	Leu	Ala	Leu	Arg	Gly
				85					90					95	

Arg	Ser	Ala	Cys	Leu	Asn	Phe	Ala	Asp	Ser	Ala	Trp	Arg	Leu	Arg	Ile
			100					105					110		

Pro	Glu	Ser	Thr	Cys	Ala	Lys	Asp	Ile	Gln	Lys	Ala	Ala	Ala	Glu	Ala
		115					120					125			

Ala	Leu	Ala	Phe	Gln	Asp	Glu	Thr	Cys	Asp	Thr	Thr	Thr	Thr	Asn	His
	130					135					140				

Gly	Leu	Asp	Met	Glu	Glu	Thr	Met	Val	Glu	Ala	Ile	Tyr	Thr	Pro	Glu
145					150					155					160

Gln	Ser	Glu	Gly	Ala	Phe	Tyr	Met	Asp	Glu	Glu	Thr	Met	Phe	Gly	Met
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165

170

175

Pro Thr Leu Leu Asp Asn Met Ala Glu Gly Met Leu Leu Pro Pro Pro  
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Ser Val Gln Trp Asn His Asn Tyr Asp Gly Glu Gly Asp Gly Asp Val  
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Ser Leu Trp Ser Tyr  
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Lys Phe Arg Glu Thr Arg His Pro Ile Tyr Arg Gly Val Arg Gln Arg
          35           40           45

Asn Ser Gly Lys Trp Val Cys Glu Leu Arg Glu Pro Asn Lys Lys Thr
          50           55           60

Arg Ile Trp Leu Gly Thr Phe Gln Thr Ala Glu Met Ala Ala Arg Ala
65           70           75           80

His Asp Val Ala Ala Ile Ala Leu Arg Gly Arg Ser Ala Cys Leu Asn
          85           90           95

Phe Ala Asp Ser Ala Trp Arg Leu Arg Ile Pro Glu Ser Thr Cys Ala
          100          105          110

Lys Glu Ile Gln Lys Ala Ala Ala Glu Ala Ala Leu Asn Phe Gln Asp
          115          120          125

Glu Met Cys His Met Thr Thr Asp Ala His Gly Leu Asp Met Glu Glu
          130          135          140

Thr Leu Val Glu Ala Ile Tyr Thr Pro Glu Gln Ser Gln Asp Ala Phe
145          150          155          160

Tyr Met Asp Glu Glu Ala Met Leu Gly Met Ser Ser Leu Leu Asp Asn
          165          170          175

Met Ala Glu Gly Met Leu Leu Pro Ser Pro Ser Val Gln Trp Asn Tyr
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Asn Phe Asp Val Glu Gly Asp Asp Asp Val Ser Leu Trp Ser Tyr
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<213> Arabidopsis thaliana

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20          25          30
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Cys Pro Lys Lys Pro Ala Gly Arg Lys Lys Phe Arg Glu Thr Arg His
35          40          45
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Pro Ile Tyr Arg Gly Val Arg Arg Arg Asn Ser Gly Lys Trp Val Cys
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Gln Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu Ala				
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Leu Arg Gly Arg Ser Ala Cys Leu Asn Phe Ala Asp Ser Ala Trp Arg				
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Leu Arg Ile Pro Glu Ser Thr Cys Ala Lys Asp Ile Gln Lys Ala Ala				
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Ala Glu Ala Ala Leu Ala Phe Gln Asp Glu Met Cys Asp Ala Thr Thr				
	130		135	140
Asp His Gly Phe Asp Met Glu Glu Thr Leu Val Glu Ala Ile Tyr Thr				
	145	150	155	160
Ala Glu Gln Ser Glu Asn Ala Phe Tyr Met His Asp Glu Ala Met Phe				
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Glu Met Pro Ser Leu Leu Ala Asn Met Ala Glu Gly Met Leu Leu Pro				
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Leu Pro Ser Val Gln Trp Asn His Asn His Glu Val Asp Gly Asp Asp				
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Asp Asp Val Ser Leu Trp Ser Tyr				
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<200>  
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 20 25 30

Phe Lys Thr Ala Glu Met Ala Ala Arg Ala His Asp Val Ala Ala Leu  
 35 40 45

Ala Leu Arg Gly Arg Gly Ala Cys Leu Asn Tyr Ala Asp Ser Ala Trp  
 50 55 60

Arg Leu Arg Ile Pro Glu Thr Thr Cys His Lys Asp Ile Gln Lys Ala  
 65 70 75 80

Ala Ala Glu Ala Ala Leu Ala Phe Glu Ala Glu Lys Ser Asp Val Thr  
 85 90 95

Met Gln Asn Gly Gln Asn Met Glu Glu Thr Thr Ala Val Ala Ser Gln  
 100 105 110

Ala Glu Val Asn Asp Thr Thr Thr Glu His Gly Met Asn Met Glu Glu  
 115 120 125

Ala Thr Ala Val Ala Ser Gln Ala Glu Val Asn Asp Thr Thr Thr Asp  
 130 135 140

His Gly Val Asp Met Glu Glu Thr Met Val Glu Ala Val Phe Thr Gly  
 145 150 155 160

Glu Gln Ser Glu Gly Phe Asn Met Ala Lys Glu Ser Thr Val Glu Ala  
165 170 175

Ala Val Val Thr Glu Glu Pro Ser Lys Gly Ser Tyr Met Asp Glu Glu  
180 185 190

Trp Met Leu Glu Met Pro Thr Leu Leu Ala Asp Met Ala Glu Gly Met  
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<220>  
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<223> n is a, c, g, or t

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